NOs:1 and 5, or the complements thereof. Support for the amendment can be found in the working Examples. More particularly, Examples 1-3 describe use of the CalA1037 probe (SEQ ID NO:1), and working Example 4 describes use of the CalA1038 probe (SEQ ID NO:5). Use of the CalA1038 probe for hybridizing nucleic acids of all of the recited yeast species is addressed on page 27 at lines 19-24. Claim 13 has also been amended to allow for the presence of an optional non-complementary sequence that does not hybridize to the recited yeast nucleic acids, and to delete the length limitation which is rendered unnecessary in view of the other amendments to the claim language. Support for this amendment can be found in the specification starting on page 14 at line 20 which states that, "...the specific probe sequences described below also may be provided in a nucleic acid cloning vector or transcript or other longer nucleic acid and still can be used for detecting *Candida albicans*, *Candida tropicalis, Candida dubliniensis, Candida viswanathii* and *Candida parapsilosis* in a highly specific manner." Claim 14 has been canceled because the limitation set forth therein is no longer relevant in view of the amendment to Claim 13. The amendment of Claim 16 to particularly recite SEQ ID NO:5 as an alternative oligonucleotide probe sequence is supported by the above-referenced disclosure on page 27 under working Example 4. The dependency of Claim 17 has been amended to conform with the cancellation of Claim 14. The amendment to Claim 25, which particularly recites SEQ ID NO:6 (the CalA1005 oligonucleotide) as an alternative helper oligonucleotide, is supported by the disclosure under working Example 4, for example in Table 4. The amendments of method Claim 26 and kit Claim 36 to depend from Claim 13, together with the amendment of Claim 27 to recite the probe sequence of SEQ ID NO:5, again are supported by the disclosure in the working Examples. The word "probe" was deleted from Claim 34 so that "said composition" would find antecedent basis in the claims from which it depends. The amendment of Claim 35 to further recite SEQ ID NO:6 as an alternative helper oligonucleotide is supported by the description of the CalA1005 oligonucleotide in working Example 4. Finally, new Claim 37 further limits the composition of Claim 13 by specifying particular alternatives for the optional non-complementary component of the recited oligonucleotide probe. Support for the amendment can be found under the definition of

"oligonucleotide probe" which appears on page 6 of the specification (see particularly page 6 starting at line 15).

No new matter is added by this Preliminary Amendment.

Entry of this Preliminary Amendment and examination of the elected claims are respectfully requested.

Restriction and Amendment of the Claims:

In response to the Restriction Requirement mailed October 1, 2002, Applicants hereby elect to pursue the invention of Group I, Claims 1-25, drawn to oligonucleotides and compositions comprising an oligonucleotide probe. Elected Claims 1-12 have been canceled to better focus prosecution of the Application. Non-elected Group II, Claims 26-36 have not been canceled. Instead, the non-elected claims have been amended to depend from the elected composition claims. Upon allowance of elected Group I claims, Applicants request rejoinder of withdrawn Group II claims, which are amended herein to have a scope commensurate with the scope of elected Claim 13. This request is made pursuant to the rules set forth under M.P.E.P. § 821.04, which states:

> Where product and process claims drawn to independent and distinct inventions are presented in the same application, applicant may be called upon under 35 U.S.C. § 121 to elect claims to either the product or process. See M.P.E.P. § 806.05(f) and § 806.05(h). The claims to the nonelected invention will be withdrawn from further consideration under 37 C.F.R. § 1.142. See M.P.E.P. § 809.02(c) and § 821 through § 821.03. *However, if applicant elects claims directed to the product, and a product claim is subsequently found allowable, withdrawn process claims which depend from or otherwise include all the limitations of the allowable product claim will be rejoined.*

With respect to prior art searching of nucleic acid sequences recited in the elected independent claim, Applicants point out that the sequence of SEQ ID NO:1 is a single nucleotide longer at its 3'-end when compared with the sequence of SEQ ID NO:5. Thus, searching of the

nucleic acid database using one query sequence should also reveal prior art relevant to the other sequence without undue burden.

CONCLUSION

The present application is now believed to be in condition for examination. Prompt examination on the merits of the application is, therefore, respectfully requested.

Respectfully submitted,

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Dated: October 31, 2002

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Appl. No. : 09/846,797
Filed : May 1, 2002

Marked-up Version of the Amended Claims

(Does not show newly added or canceled claims)

13. **(Amended)** A composition for detecting the nucleic acids of a yeast that is any of *C. albicans*, *C. tropicalis*, *C. dubliniensis*, *C. viswanathii* and *C. parapsilosis*, said composition comprising an oligonucleotide probe having **[a sequence, said sequence comprising the]** the length and sequence of SEQ ID NO:1 or the complement thereof or the length and sequence of SEQ ID NO:5 or the complement thereof, and optionally a non-complementary sequence that does not hybridize to the nucleic acids of said yeast**[, said oligonucleotide probe having a length of up to 100 nucleotide bases]**.

16. **(Amended)** The composition of Claim 13, wherein the sequence of said oligonucleotide probe consists of SEQ ID NO:1 or SEQ ID NO:5.

17. **(Amended)** The composition of Claim **[14]** 13, wherein said oligonucleotide probe further comprises a detectable label.

25. **(Amended)** The composition of Claim 22, wherein said at least one helper oligonucleotide has a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, **[and]** SEQ ID NO:4 and SEQ ID NO:6.

26. **(Amended)** A method of determining whether an organism in the genus *Candida* is present in a test sample, said method comprising the steps of:

(a) providing to said test sample a **[probe]** composition **[comprising an oligonucleotide probe having a sequence, said sequence comprising SEQ ID NO:1, said oligonucleotide probe having a length of up to 100 nucleotide bases]** in accordance with Claim 13;

(b) hybridizing under a high stringency condition any nucleic acid that may be present in the test sample with said **[probe]** composition to form a probe:target duplex; and

(c) detecting said probe:target duplex, whereby it is determined that an organism that is any of *C. albicans*, *C. tropicalis*, *C. dubliniensis*, *C. viswanathii* and *C. parapsilosis* is present in the test sample.

27. **(Amended)** The method of Claim 26, wherein the sequence of said oligonucleotide probe in step (a) consists of SEQ ID NO:1 or SEQ ID NO:5.

34. **(Amended)** The method of Claim 32, wherein said **[probe]** composition in step (a) further comprises at least one helper oligonucleotide.

35. **(Amended)** The method of Claim 34, wherein said at least one helper oligonucleotide is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, **[and]** SEQ ID NO:4, and SEQ ID NO:6.

36. **(Amended)** A kit for detecting the presence of nucleic acids from any of *C. albicans*, *C. tropicalis, C. dubliniensis, C. viswanathii* and *C. parapsilosis* in a test sample, said kit comprising:

(a) a composition **[comprising a detectably labeled oligonucleotide probe having the sequence of SEQ ID NO:1]** in accordance with Claim 13; and

(b) at least one helper oligonucleotide.